

AMENDMENTS TO THE SPECIFICATION

Please replace the sequence alignment table beginning on page 16, line 13, and bridging to page 18, line 34, with the following amended sequence alignment table:

Nucleic acid alignment for SEQ ID NOS. 1, 3, 5, 7, and 9:

| | | | |
|--------------|-------|---|-----|
| 1 | | | 50 |
| CanA | (1) | GTGAAGTACACAACCCCTAGCTATAGCGGGTATTATTGCCTCGGCTGCCGC | |
| CanB | (1) | GTGAAGCCTACGGCTCTAGCCCTGGCTGGTATCATTGCCTCGGCTGCCGA | |
| CanC | (1) | ATGAGGTACACGACCCTAGCTCTGGCCGGCATAGTGGCTCGGCTGCCGC | |
| CanD_partial | (1) | ----- | |
| CanE_partial | (1) | ----- | |
| Consensus | (1) | TGA G AC C CTAGC T GC GG AT T GCCTCGGCTGCCG | |
| | | 51 | 100 |
| CanA | (51) | CCTCGCCCTCCTAGCAGGCTTCGCCACCAACCCAGAGCCCCCTCAACAGCT | |
| CanB | (51) | CCTCGCCCTGCTAGCAGGCTTCGCCACCAACCCAGAGCCCGCTCAACAGCT | |
| CanC | (51) | CCTCGCCCTGCTAGCAGGCTTCGCCACGACCCAGAGCCCGCTAAGCAGCT | |
| CanD_partial | (1) | -----AGCT | |
| CanE_partial | (1) | -----AGCT | |
| Consensus | (51) | CCTCGCCCT CTAGCAGGCTTCGCCAC ACCCAGAGCCC CT A CAGCT | |
| | | 101 | 150 |
| CanA | (101) | TCTACGCCACCGGTACAGCACAGGCAGTAAGCGAGCCAATAGACGTAGAA | |
| CanB | (101) | TCTACGCCACCGGCACAGCAGCCGCAACAAGCGAGCCAATAGACGTAGAG | |
| CanC | (101) | TCTACGCCACCGGCACAGCACAAGCAGTAAGCGAGCCAATAGACGTAGAG | |
| CanD_partial | (5) | TCTACGCCACCGGCACAGCACAGGCAGTAAGCGAGCCAATAGACGTGGTA | |
| CanE_partial | (5) | TCTACGCCACCGGCACAGCAGAGGCAACAAGCGAGCCAATAGACGTTGTA | |
| Consensus | (101) | TCTACGCCACCGGCACAGCACAGGCAGTAAGCGAGCCAATAGACGTAGAA | |
| | | 151 | 200 |
| CanA | (151) | AGCCACCT---CGGCAGCATAACCCCCGAGCCGGCGCACAGGGCAGTGA | |
| CanB | (151) | AGCCACCT---CAGCAGCATAGCCCCTGCTGCTGGCGCACAGGGCAGCCA | |
| CanC | (151) | AGCCACCTAGACAACACCATAGCCCCTGCTGCCGGTGACACAGGGCTACAA | |
| CanD_partial | (55) | AGCAGCCTCGGTACG---CTAAATACTGCCGCTGGTGACACAGGGTAAGCA | |
| CanE_partial | (55) | AGCAACCTTAACACGGCCATAGCCCCTGCTGCCGGCGCCCAGGGCAGCGT | |
| Consensus | (151) | AGCCACCT CA CA CATAGCCCCTGCTGCCGGCGCACAGGGCAGC A | |
| | | 201 | 250 |
| CanA | (198) | CGACATAGGTTACGCAATAGTGTGGATAAAGGACCAGGTCAATGATGTAA | |
| CanB | (198) | GGACATAGGCTACTTCAACGTGACCGCCAAGGATCAAGTGAACGTGACAA | |
| CanC | (201) | GGACATGGGCTACATTAAGATAACTAACCAGTCAAAAGTTAATGTAATAA | |
| CanD_partial | (102) | GACGCTAGGAGACATAACAATATATGCGCACAATGACGTGAACATAACAA | |
| CanE_partial | (105) | GGGCATAGGCAGCATAACAATAGAGAACAAGACTGACGTGAACGTTGTGA | |
| Consensus | (201) | GGACATAGGCTACATAA AATA A CAAG AT A GTGAACGT ATAA | |
| | | 251 | 300 |
| CanA | (248) | AGCTGAAGGTGACCCTGCGTAACGCTGAGCAGCTAAAGCCCTACTTCAAG | |
| CanB | (248) | AGATAAAGGTGACCCTGGCTAACGCTGAGCAGCTAAAGCCCTACTTCAAG | |
| CanC | (251) | AGCTGAAGGTGACTCTCGCTAACGCCGAGCAGCTAAAGCCCTACTTGCAC | |
| CanD_partial | (152) | AGCTAAAGGTACGCTTGCTAACGCTGCACAGCTAAGACCATACTTCAAG | |
| CanE_partial | (155) | AGCTGAAGATAACCCTCGCCAACGCTGAGCAGCTAAAGCCCTACTTGCAC | |
| Consensus | (251) | AGCTGAAGGTGACCCT GCTAACGCTGAGCAGCTAAAGCCCTACTTCAAG | |
| | | 301 | 350 |
| CanA | (298) | TACCTACAGATACAGATAACAAGCGGCTATGAGACGAACAGCACAGCTCT | |
| CanB | (298) | TACCTACAGATAGTGCTAAAGAGCG----- | |
| CanC | (301) | TACCTACAGCTAGTACTCACAAGCAAC-----GCCAC | |
| CanD_partial | (202) | TACCTGATAATAAAGCTAGTAAGCCT-----GGACAGC-AA | |
| CanE_partial | (205) | TACCTACAGATAGTGCTAAAGAGCGT-----TGACAGC-AA | |

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Consensus (301) TACCTACAGATAGTGCTAA AAGCG ACAGC A
351 400
CanA (348) AGGCAACTTCAGCGAGACCAAGGCTGTGATAAGCCTCGACAACCCAGCG
CanB (323) AGGTAGCTGA--CGAGATCAAGGCCGTAATAAGCATAGACAAGCCTAGCG
CanC (333) TGGCACCGACA---TGGTTAAGGCTGTGCTAAGCCTCGAGAAGCCTAGCG
CanD_partial (237) CGGCAACGAGTCCGAGGAAAAGGGCATGATAACTCTATGGAAGCCTTACG
CanE_partial (240) CGAGATCAAGGCTG-----TGCTAAGCCTCGAGAAGCCAGCG
Consensus (351) GGCA C A CGAG AAGGC GTGATAAGCCTCGAGAAGCCTAGCG
401 450
CanA (398) CCGTGATAGTACTAGACAAGGAGGATATAGCAGTGCTCTATCCGGACAAG
CanB (371) CCGTCATAATACTAGACAGCCAGGA-----
CanC (380) CAGTCATAATACTAGACAACGATGA-----
CanD_partial (287) CCGTGATAATACTAGACCATGAAGA-----
CanE_partial (278) CAGTCATAATACTGGACAACGAGGA-----
Consensus (401) CCGTCATAATACTAGACAACGAGGA
451 500
CanA (448) ACCGGTTACACAAACACTTCGATATGGGTACCCGGTGAACCTGACAAGAT
canB (396) -----CTTCGACA-----G-----
CanC (405) -----CTACGATA-----G-----
canD_partial (312) -----TTTCAACAACGACA-----
canE_partial (303) -----CTTCAGGGCGGC-----
Consensus (451) CTTCGA A G
501 550
CanA (498) AATTGTCTACAACGAGACAAAGCCAGTAGCTATACTGAACTTCAAGGCCT
canB (405) -----CAACAACAGAGCAAAG--ATAAGCGCCACTG-----CCT
CanC (414) -----CACTAACAAGATACAGCTA--AAGGTAGA---A-----G-CCT
canD_partial (326) -----TCGACAATGACGGCAACAATGACGCCAAGATAAGGGTTGTAGCCT
canE_partial (316) -----GACAACCAAGTGCCAGATAGACGCCACC-----GCCT
Consensus (501) C ACAAC AG AAAG AGAAGC A A T A GCCT
551 600
CanA (548) TCTACGAGGCTAAGGAGGGTATGCTATTTCGACAGCCTGCCAGTGATATTC
canB (437) ACTACGAGGCTAAGGAGGGCATGCTATTTCGACAGCCTACCGCTAATATTC
CanC (446) ACTATGAGGCTAAGGAGGGCATGCTATTTCGACAGCCTACCAGTAATACTG
canD_partial (371) ACTATGAGGCTAAGGAGGGTATGCT-----
canE_partial (347) ACTACGAGGCTAAGGAGGGTATGCTA-----
Consensus (551) ACTACGAGGCTAAGGAGGGTATGCTATTTCGACAGCCT CC T ATA T
601 642
CanA (598) AACTTCCAGGTGCTACAAGTAGGCTAA-----
canB (487) AACATACAGGTGCTAAGCGTCAGCTAA-----
CanC (496) AACTTCCAGGTACTGAGCGCCGCTTGACAGTCCCTTGTGGTGA
canD_partial (396) -----
canE_partial (373) -----
Consensus (601) AAC T CAGGT CT G T

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Amino Acid Alignment for SEQ ID NOS. 2, 4, 6, 8, and 10:

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1 50
CanA_pep (1) VKYTTLAIAGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVE
CanB_pep (1) VKPTALALAGIIASAADLALLAGFATTQSPLNSFYATGTAAATSEPIDVE
CanC_pep (1) MRYTTLALAGIVASAAALALLAGFATTQSPLSSFYATGTAQAVSEPIDVE
CanD_partial (1) -----SFYATGTAQAVSEPIDVV
CanE_partial (1) -----SFYATGTAEATSEPIDVV
Consensus (1) VK T LALAGIIASAA LALLAGFATTQSPL SFYATGTAQAVSEPIDVE
51 100
CanA_pep (51) SHLG-SITPAAGAQQSDDIGYAIVWIKDQVNDVKLVTLRNAEQLKPYFK
CanB_pep (51) SHLS-SIAPAAGAQQSQDIGYFNVTAQDQVNVTKIKVTLANAEQLKPYFK
CanC_pep (51) SHLDNTIAPAAGAQQYKDMGYIKITNQSKVNVIKLVTLANAEQLKPYFD
CanD_partial (19) SSLGTLNT-AAGAQQKQTLGDITIIYAHNDVNITKLVTLANAAQLRPYFK

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CanE_partial (19) SNLNTAIAPAAGAQGSVGIGSITIENKTDVNVVKLKITLANAEQLKPYFD
Consensus (51) SHL SIAPAAGAQGS DIGYI I K VNVVKLVITLANAEQLKPYFK
                101                                150
CanA_pep (100) YLQIQITSGYETNSTALGNFSETRKAVISLDNPSAVIVLDKEDIAVLYPDK
CanB_pep (100) YLQIVLKSEVAD-----EIKAVISIDKPSAVIILDSQDFDSNNR--
CanC_pep (101) YLQLVLTSNATG-----TDMVKAVLSLEKPSAVIILDNDYDSTN---
CanD_partial (68) YLIIKLVSLSNG-----NESEEKGMITLWKPYAVIILDHEDFNNDID--
CanE_partial (69) YLQIVLKSVDN-----EIKAVLSLEKPSAVIILDNEDFQG-----
Consensus (101) YLQIVL S S EIKAVISLDKPSAVIILD EDF
                151                                200
CanA_pep (150) TGYTNTSIWVPGEPDKIIVYNETKPVAILNFKAFYEAKEGMLFDSLPLVIF
CanB_pep (139) -----AKISATAYYEAKEGMLFDSLPLIF
CanC_pep (141) -----KIQ-----LKVEAYYEAKEGMLFDSLPLVIL
CanD_partial (111) -----N--DGNNDAKIRVVAYYEAKGML-----
CanE_partial (105) -----GDNQCQIDATAYYEAKEGML-----
Consensus (151) A I AYYEAKEGMLFDSLPLVI
                201                214
CanA_pep (200) NFQVLQVG-----
CanB_pep (163) NIQVLSVS-----
CanC_pep (166) NFQVLSAACSPLW-
CanD_partial (132) -----
CanE_partial (125) -----
Consensus (201) N QVL

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